

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 11:43:18 ; Search time 66 Seconds
(without alignments)
69.699 Million cell updates/sec

Title: US-09-648-389A-1

Perfect score: 15

Sequence: 1 cttggccgctgccat 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents,NA:*

1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*

2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*

3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*

4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*

5: /cgn2_6/ptodata/2/1na/PCNUS.COMB.seq:*

6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	4	US-09-142-779-4
2	15	100.0	843	1	US-08-040-548-9
3	15	100.0	843	1	US-08-466-344-9
4	15	100.0	3068	2	US-08-224-482-1
5	15	100.0	3086	1	US-08-040-548-15
6	15	100.0	3086	1	US-08-466-344-15
7	15	100.0	3086	6	5206152-1
8	13.4	89.3	25	2	US-08-626-169-12
9	13.4	89.3	25	3	US-09-164-907-12
10	13.4	89.3	612	2	US-08-760-075A-15
11	13.4	89.3	612	4	US-09-338-546-15
12	13.4	89.3	612	4	US-09-659-084-15
13	13.4	89.3	724	4	US-08-858-207A-206
14	13.4	89.3	1920	2	US-08-855-714-1
15	13.4	89.3	2291	1	US-07-872-644-5
16	13.4	89.3	2291	1	US-08-297-494-5
17	13.4	89.3	2291	1	US-08-297-510-5
18	13.4	89.3	2291	1	US-08-479-532-5
19	13.4	89.3	2291	1	US-08-455-526-5
20	13.4	89.3	2291	1	US-08-455-526-5
21	13.4	89.3	2291	3	US-09-139-491-5
22	13.4	89.3	2291	5	PCR-US92-03222-5
23	13.4	89.3	2656	1	US-07-872-644-16
24	13.4	89.3	2656	1	US-08-297-494-16
25	13.4	89.3	2656	1	US-08-297-510-16
26	13.4	89.3	2656	1	US-08-479-532-16
27	13.4	89.3	2656	1	US-08-455-526-16

28	13.4	89.3	2656	1	US-08-455-525-16	Sequence 16, Appl
29	13.4	89.3	2656	3	US-09-139-491-16	Sequence 16, Appl
30	13.4	89.3	2656	5	PCR-US92-03222-16	Sequence 16, Appl
31	13.4	89.3	2781	1	US-08-178-477B-42	Sequence 42, Appl
32	13.4	89.3	3132	2	US-08-224-482-3	Sequence 3, Appl
33	13.4	89.3	3132	3	US-09-205-921-1	Sequence 1, Appl
34	13.4	89.3	3539	3	US-08-936-135-7	Sequence 1, Appl
35	13.4	89.3	4718	3	US-08-936-135-9	Sequence 1, Appl
36	13.4	89.3	4733	3	US-08-936-135-11	Sequence 11, Appl
37	13.4	89.3	4765	3	US-08-936-135-21	Sequence 21, Appl
38	13.4	89.3	4769	3	US-08-936-135-13	Sequence 13, Appl
39	13.4	89.3	4772	4	US-09-484-970B-133	Sequence 133, Appl
40	13.4	89.3	4780	3	US-08-936-135-23	Sequence 23, Appl
41	13.4	89.3	4784	3	US-08-936-135-15	Sequence 15, Appl
42	13.4	89.3	28171	4	US-08-961-5527-22	Sequence 22, Appl
43	13.4	89.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl
44	13	86.7	25	4	US-09-257-583-30	Sequence 30, Appl
45	13	86.7	614	2	US-07-625-334-1	Sequence 1, Appl

ALIGNMENTS

```

RESULT 1
US-09-142-779-4
: Sequence 4, Application US/09142779B
: Patent No. 6200960
: GENERAL INFORMATION:
: APPLICANT: Knachigian, Levon M.
: TITLE OF INVENTION: Inhibition of Proliferation of Cells
: FILE REFERENCE: 273402002000
: CURRENT APPLICATION NUMBER: US/09/142,779B
: EARLIER FILING DATE: 1999-04-13
: EARLIER APPLICATION NUMBER: PR 8554
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 15
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Oligonucleotide
US-09-142-779-4

Query Match      100.0%  Score 15;  DB 4;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 42;
Matches 15;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

DB      1  CTTGGCCGCTGCCAT 15
      1  CTTGGCCGCTGCCAT 15

RESULT 2
US-08-040-548-9/c
: Sequence 9, Application US/08040548
: Patent No. 5763209
: GENERAL INFORMATION:
: APPLICANT: Sukhatme, Vikas P.
: TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
: TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
: NUMBER OF SEQUENCES: 67
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: 321 No. 5763209th Clark Street, Suite 800
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60610
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

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/ TITLE OF INVENTION: Molecular Toxicology Modeling
/ FILE REFERENCE: 44921-5038-US
/ CURRENT APPLICATION NUMBER: US/09/917,800A
/ CURRENT FILING DATE: 2001-07-31
/ PRIOR APPLICATION NUMBER: US 60/222,040
/ PRIOR FILING DATE: 2000-07-31
/ PRIOR APPLICATION NUMBER: US 60/222,880
/ PRIOR FILING DATE: 2000-11-02
/ PRIOR APPLICATION NUMBER: US 60/290,029
/ PRIOR FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: US 60/290,645
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: US 60/292,336
/ PRIOR FILING DATE: 2001-05-22
/ PRIOR APPLICATION NUMBER: US 60/295,798
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: US 60/297,457
/ PRIOR FILING DATE: 2001-06-13
/ PRIOR APPLICATION NUMBER: US 60/298,884
/ PRIOR FILING DATE: 2001-06-19
/ PRIOR APPLICATION NUMBER: US 60/303,459
/ PRIOR FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 1740
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 1543
/ LENGTH: 3112
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012551
US-09-917-800A-1543
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Query Match          100.0%; Score 15; DB 10; Length 3112;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CTTGGCCGCTGCCAT 15
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DB 283 CTTGGCCGCTGCCAT 269
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RESULT 3
US-09-974-300-5464/C
/ Sequence 5464, Application US/09974300
/ Patent No. US20020146721A1
/ GENERAL INFORMATION:
/ APPLICANT: Berka, Randy M.
/ APPLICANT: Clausen, Ib Groth
/ TITLE OF INVENTION: Methods For Monitoring Multiple Gene
/ TITLE OF INVENTION: Expression
/ FILE REFERENCE: 10085, 500-US
/ CURRENT APPLICATION NUMBER: US/09/974,300
/ CURRENT FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 09/680,598
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/279,526
/ PRIOR FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 8481
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 5464
/ LENGTH: 152
/ TYPE: DNA
/ ORGANISM: Bacillus clausii
US-09-974-300-5464
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Query Match          89.3%; Score 13.4; DB 10; Length 152;
Best Local Similarity 93.3%; Pred. No. 2,5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 CTTGGCCGCTGCCAT 15
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DB 49 CTTGGCCGCTGCCAT 35
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RESULT 4
US-09-864-761-27552
/ Sequence 27552, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
/ FILE REFERENCE: Aecm1ca-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263,6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
/ SEQ ID NO: 27552
/ LENGTH: 157
/ TYPE: DNA
/ ORGANISM: Homo sapiens
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FEATURE:
/ OTHER INFORMATION: MAP TO AC003108.1
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
/ OTHER INFORMATION: NT HIT: M64229.1, EVALU2.30e-02
/ OTHER INFORMATION: EST_HUMAN HIT: BE85401.1, EVALU2.00e-83
US-09-864-761-27552
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Query Match          89.3%; Score 13.4; DB 10; Length 157;
Best Local Similarity 93.3%; Pred. No. 2,5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: 321 No. 5763209th Clark Street, Suite 800
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: U.S.A.
;; ZIP: 60610
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/040,548
;; FILING DATE:
;; CLASSIFICATION: 514
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coughlin, Daniel F.
;; REGISTRATION NUMBER: 36,111
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 744-0090
;; TELEFAX: (312) 245-4961
;;
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3086 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;;
;; US-08-040-548-15

Query Match 100.0%; Score 15; DB 1; Length 3086;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
 |||||
Db 273 CTTGGCCGCTGCCAT 259

;; RESULT 6
;; US-08-466-344-15/C
;; Sequence 15, Application US/08466344
;; Patent No. 5773583
;; GENERAL INFORMATION:
;; APPLICANT: Sukhatme, Vikas P.
;; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
;; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
;; NUMBER OF SEQUENCES: 67
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: 321 No. 5773583th Clark Street, Suite 800
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: U.S.A.
;; ZIP: 60610
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/466,344
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 514
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/040,548
;; FILING DATE: 31-MAR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coughlin, Daniel F.
;; REGISTRATION NUMBER: 36,111
;; REFERENCE/DOCKET NUMBER: arcd067

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 744-0090
;; TELEFAX: (312) 245-4961
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3086 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;;
;; US-08-466-344-15

Query Match 100.0%; Score 15; DB 1; Length 3086;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
 |||||
Db 273 CTTGGCCGCTGCCAT 259

;; RESULT 7
;; 5206152-1/C
;; Patent No. 5206152
;; APPLICANT: SUKHATME, VIKAS P.
;; TITLE OF INVENTION: CLONING AND EXPRESSION OF EARLY GROWTH
;; REGULATORY PROTEIN GENES
;; NUMBER OF SEQUENCES: 18
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/249,584
;; FILING DATE: 26-SEP-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 179,587
;; FILING DATE: 08-APR-1988
;; SEQ ID NO:1:
;; LENGTH: 3086
;;
;; 5206152-1

Query Match 100.0%; Score 15; DB 6; Length 3086;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
 |||||
Db 273 CTTGGCCGCTGCCAT 259

;; RESULT 8
;; US-08-626-169-12/C
;; Sequence 12, Application US/08626169
;; Patent No. 5861248
;; GENERAL INFORMATION:
;; APPLICANT: Russell, David W.
;; TITLE OF INVENTION: Thapsigen, Anice E.
;; TITLE OF INVENTION: BIOMARKERS FOR DETECTION, DIAGNOSIS
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: United States
;; ZIP: 77210
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/626,169
;; FILING DATE: Concurrently Herewith
;; CLASSIFICATION: 435

OTHER INFORMATION: SWISSPROT HIT: P48651, EVALUE 6.80e+00
OTHER INFORMATION: NT HIT: X74507.1, EVALUE 6.10e-01
US-09-864-761-31839

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 10; Length 255;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
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DB 66 CTTGGCCTGCTGCCAT 52

RESULT 7
US-09-923-876-2313/c
Sequence 2313, Application US/09923876
Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Laligudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)

FILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

PRIOR APPLICATION NUMBER: 09/298,329

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 60/085,331

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL Program

SEQ ID NO 2313

LENGTH: 265

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20020013958A1 700160401H1

LOCATION: 48

OTHER INFORMATION: a, t, c, g, or other

US-09-923-876-2313

Query Match

Best Local Similarity 89.3%; Score 13.4; DB 10; Length 265;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
|||||
DB 70 CTTGGCCTGCTGCCAT 56

RESULT 8
US-09-923-876-4805/c

Sequence 4805, Application US/09923876

Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Laligudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)

FILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

PRIOR APPLICATION NUMBER: 09/298,329

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 60/085,331

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL Program

SEQ ID NO 4805

LENGTH: 273

TYPE: DNA

ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700455822H1
US-09-923-876-4805

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 10; Length 273;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
|||||
DB 270 CTTGGCCTGCTGCCAT 256

RESULT 9
US-09-960-352-4856/c

Sequence 4856, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengping

FILE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 4856

LENGTH: 349

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 21-LIB34-001-Q1-E1-F9

US-09-960-352-4856

Query Match

Best Local Similarity 89.3%; Score 13.4; DB 10; Length 349;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
|||||
DB 48 CTTGGCCGCTGCCAT 34

RESULT 10
US-09-960-352-11961/c

Sequence 11961, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.

FILE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 11961

LENGTH: 414

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 51-LIB34-004-Q1-E1-E4

US-09-960-352-11961

Query Match

Best Local Similarity 89.3%; Score 13.4; DB 10; Length 414;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15

ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..612
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..612
US-09-338-546-15

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 4; Length 612;
Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCACAT 15
Db 339 CTTGGCCGCTGCACAT 325

RESULT 12
US-09-659-084-15/c
Sequence 15, Application US/09659084
Patent No. 6403299

GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
MODELNER, Stefan
BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/659,084
FILING DATE: 11-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/338,546
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..612
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..612
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-659-084-15

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 4; Length 612;
Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCACAT 15
Db 339 CTTGGCCGCTGCACAT 325

RESULT 13
US-08-858-207A-206
Sequence 206, Application US/08858207A
Patent No. 6348328

GENERAL INFORMATION:
APPLICANT: Black, Michael
Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328e1 Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmli, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-858-207A-206

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 4; Length 724;
Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCACAT 15
Db 367 CTTGGCCGCTGCACAT 381

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;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 16568
;; LENGTH: 454
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC007263.3
;; OTHER INFORMATION: EXPRESSED IN BR474, SIGNAL = 0.64
US-09-864-761-16568
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Query Match      89.3%; Score 13.4; DB 10; Length 454;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CTGGCCCTGCCAT 15
Db 346 CTGGCTGCTGCCAT 332
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RESULT 14
US-09-864-761-10916
;; Sequence 10916, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aesomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263,6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
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;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 10916
;; LENGTH: 480
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC003108.1
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
US-09-864-761-10916
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```
Query Match      89.3%; Score 13.4; DB 10; Length 480;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CTGGCCCTGCCAT 15
Db 413 CTGGCAGCTGCCAT 427
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```
RESULT 15
US-09-974-300-5449/c
;; Sequence 5449, Application US/09974300
;; Patent No. US20020146721A1
;; GENERAL INFORMATION:
;; APPLICANT: Berka, Randy M.
;; APPLICANT: Clausen, Ib Groth
;; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
;; FILE REFERENCE: 10085,500-US
;; CURRENT APPLICATION NUMBER: US/09/974,300
;; CURRENT FILING DATE: 2001-10-05
;; PRIOR APPLICATION NUMBER: 09/680,598
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 60/279,526
;; PRIOR FILING DATE: 2001-03-27
;; NUMBER OF SEQ ID NOS: 8481
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5449
;; LENGTH: 489
;; TYPE: DNA
;; ORGANISM: Bacillus clausii
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(489)
;; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5449
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Query Match      89.3%; Score 13.4; DB 10; Length 489;
```

CC Vascular cells, preferably smooth muscle or endothelial cells or cells
 CC involved in neoplasia.
 XX

SO Sequence 4321 BP; 908 A; 1308 C; 1106 G; 999 T; 0 other;

Query Match 100.0%; Score 15; DB 21; Length 4321;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||
 DB 828 CTTGGCCGCTGCCAT 814

RESULT 13

AAAF85131/C
 ID AAAF85131 standard; DNA; 4321 BP.

XX
 AC AAAF85131;

DT 09-JUL-2001 (first entry)

DE Nucleotide sequence of rat early growth response factor-1.

XX Early growth response factor; EGR; tumour cell; tumour; DNazyme;
 KM antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
 KM skin carcinoma; breast tumour; ss.

XX Rattus rattus.

XX WO20010394-A1.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-AU01315.

XX 26-OCT-1999; 99AU-0003676.

XX (UNIX) UNISEARCH LTD.

XX Khachigian LM;

XX WPI: 2001-300428/31.

XX Treating tumors including prostate tumour, breast tumour, skin carcinoma,
 PT comprising administering agent which inhibits induction or decreases
 PT expression of early growth response factor-1

XX Disclosure: Page 16-23; 80pp; English.

XX The present sequence represents an early growth response factor-1
 CC (EGR-1) DNA sequence. The specification describes a method for
 CC inhibiting the growth or proliferation of a tumour cell and treating
 CC tumours. The method comprises contacting a tumour cell or administering
 CC to a subject, an agent which inhibits induction, decreases expression
 CC or which decreases the nuclear accumulation or activity of EGR. The
 CC agent is a DNazyme or an antisense oligonucleotide. The method is
 CC useful for treating solid tumours, including prostate tumours,
 CC hepatocellular carcinoma, skin carcinoma or breast tumours.
 XX

SO Sequence 4321 BP; 908 A; 1308 C; 1106 G; 999 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 4321;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||
 DB 828 CTTGGCCGCTGCCAT 814

RESULT 14

AB199867/c

ID AB199867 standard; CDNA; 4494 BP.

XX
 AC AB199867;

DT 07-MAR-2002 (first entry)

DE Mouse ischemic condition related CDNA sequence SEQ ID NO:1002.

XX Mouse; ischemia; compressive ischemia; occlusive ischemia;
 KM vasospastic ischemia; ischemic condition; ischemic disease; ss.

XX Mus musculus.

XX WO20018188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP04192.

XX 18-MAY-2000; 2000JP-0145977.

XX (UNIT) UNITV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI: 2002-034733/04.

XX P-PSDB; ABB57356.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or
 PT by determining the expression profile of a gene group comprising these
 PT genes

XX Claim 2; Page 2532-2537; 2690pp; English.

XX The present invention describes a method for examining ischemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischemic condition (e.g. compressive
 CC ischemia, occlusive ischemia or vasospastic ischemia) by measuring
 CC expression levels of particular genes (AB199202 to AB199912, encoding
 CC the protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The
 CC expression levels or expression profiles produced by these genes are
 CC used as an indicator when screening for ischemic condition-improving
 CC drugs or therapeutics for ischemic diseases. AB19913 and AB19914
 CC represent PCR primers for a mouse ischemic condition related sequence,
 CC which are used in the exemplification of the present invention.
 XX

SO Sequence 4494 BP; 940 A; 1417 C; 1163 G; 974 T; 0 other;

Query Match 100.0%; Score 15; DB 24; Length 4494;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||
 DB 1692 CTTGGCCGCTGCCAT 1678

RESULT 15

ABN17030/c
 ID ABN17030 standard; CDNA; 501 BP.

XX
 AC ABN17030;

DT 24-JUN-2002 (first entry)

DE Human ORFX polynucleotide sequence SEQ ID NO:2537.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KM hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001).
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers

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1..459
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_id="RIKEN full-length enriched, pooled cell lines"
/note="Pooled cell lines ; (cell_line=RCB-1751 WEHI 164),
(cell_line=CRL-2116 JC), (cell_line=RCB-0035 WEHI-3),
(cell_line=RCB-0464 Meth-A), (cell_line=RCB-0545 OHTA),
(cell_line=RCB-0559 K-1.F1), (cell_line=RCB-1283 B16
melanoma), (cell_type=B cells, cell_line=CRL-1702 WEHI 231
), (cell_type=Leydig cells, cell_line=CRL-2065 MTC-1),
(cell_type=Nullipotent stem cell, cell_line=CRL-2070 NE),
(tissue_type=bladder, cell_line=RCB-0544 MBF-2),
(tissue_type=bone marrow, cell_type=stroma cell,
cell_line=CRL-2028 SR-4987), (tissue_type=colon,
cell_line=RCB-0549 C1e-H3), (tissue_type=kidney,
cell_line=CCL-142 RAG), (tissue_type=submandibular gland,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/c,
cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20-3b3
), (strain=C3H, tissue_type=brain, cell_line=CRL-1443
BC3H1)"
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BASE COUNT 82 a 172 c 136 g 69 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 15; DB 10; Length 459;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGGCCGCTGCCAT 15

Db 300 CTTGGCCGCTGCCAT 286

Search completed: December 16, 2002, 14:15:28
Job time : 2426 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: December 16, 2002, 11:04:08 : Search time 303 Seconds

(without alignments)
11.485 Million cell updates/sec

Title: US-09-648-389A-1

Perfect score: 15

Sequence: 1 ctggccgcgtccat 15

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.GeneSeq.101002:*

1: /SID2/gcgdata/geneSeq/geneSeq-emb1/NA1980.DAT:*

2: /SID2/gcgdata/geneSeq/geneSeq-emb1/NA1981.DAT:*

3: /SID2/gcgdata/geneSeq/geneSeq-emb1/NA1982.DAT:*

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6: /SID2/gcgdata/geneSeq/geneSeq-emb1/NA1985.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15	100.0	15 18 AAT90567	Antisense sequence
2	15	100.0	15 21 AAA74448	Rat AS2 sequence
3	15	100.0	15 22 AAF85119	Antisense oligonuc
4	15	100.0	15 22 AAF85133	Antisense oligonuc
5	15	100.0	843 15 AAO73457	Egr-1 transcriptio
6	15	100.0	3068 20 AAIV64275	Mouse Egr-1 CDNA
7	15	100.0	3068 21 AAA74395	Mouse Egr-1 coding
8	15	100.0	3068 22 AAF85130	Nucleotide sequenc
9	15	100.0	3086 10 AAN91815	Egr-1-contg. OC3.1

10	15	100.0	3086 15 AAO73463	Mouse Egr-1 clone
11	15	100.0	3112 24 ABR63636	Rat sequence diffe
12	15	100.0	4321 21 AAA74396	Rat Egr-1 coding s
13	15	100.0	4321 22 AAF85131	Nucleotide sequenc
14	15	100.0	4494 24 ABI199867	Mouse ischaemic co
15	14	93.3	501 24 ABN17030	Human OREF polynuc
16	14	93.3	987 23 AAS92184	Human encoding novel
17	14	93.3	1566 21 AAC42849	Arabidopsis thalia
18	14	93.3	2100 22 AAH66705	C glutamic codin
19	14	93.3	2223 22 AAF71483	Corynebacterium g1
20	14	93.3	2350 22 AAS15846	C. glutamicum pat
21	14	93.3	2588 21 AAC76756	Human OREF ORF2311
22	14	93.3	3192 22 AAL04902	Human reproductive
23	14	93.3	3192 23 AAL04903	Human testicular a
24	14	93.3	3192 23 ABL97796	Human testicular a
25	14	93.3	3192 23 ABL97797	Drosophila melanog
26	14	93.3	3479 23 ABL06683	DNA encoding Coryn
27	14	93.3	4108 22 AAF99988	Nucleotide sequenc
28	14	93.3	6995 22 AAF25332	C. glutamicum Opca
29	14	93.3	6995 22 AAF25332	Drosophila melanog
30	14	93.3	9863 23 ABL20890	Drosophila melanog
31	14	93.3	13497 23 ABL03557	Drosophila melanog
32	14	93.3	13497 23 ABL03557	Drosophila melanog
33	14	93.3	15464 23 ABL06682	Drosophila melanog
34	14	93.3	16489 23 ABL03556	Drosophila melanog
35	14	93.3	349980 22 AAF68529	C glutamicum codin
36	13.4	89.3	25 18 AAT89069	Identification of
37	13.4	89.3	152 24 ABR78173	Bacillus clausii g
38	13.4	89.3	157 22 ABR70430	Human foetal liver
39	13.4	89.3	157 22 AAK18671	Human brain expres
40	13.4	89.3	157 22 AAK44600	Human bone marrow
41	13.4	89.3	157 22 AAI50582	Probe #19268 used
42	13.4	89.3	157 24 ABS18838	Human genome-deriv
43	13.4	89.3	174 21 AAC20671	Human secreted pro
44	13.4	89.3	197 22 AAL19770	Human breast cance
45	13.4	89.3	200 22 AAL19820	Human breast cance

ALIGNMENTS

RESULT 1

AAT90567

AAT90567 standard; DNA; 15 BP.

AC AAT90567;

XX 24-MAR-1998 (first entry)

DE Antisense sequence A/S2 directed against Egr-1.

DE Antisense sequence: Inhibitor; Egr-1; rat; early growth response gene;

KW cellular proliferation; Inhibitor; cell migration inhibition; therapy;

KW atherosclerosis; restenosis; ss.

XX Synthetic.

OS Rattus sp.

OS W09732979-A1.

PN 12-SEP-1997.

PD 07-MAR-1997; 97WO-AU00140.

PF 07-MAR-1997; 97WO-AU00140.

PR 07-MAR-1996; 96AU-0008554.

PA (UNIX) UNISEARCH LTD.

XX Khachigian LM;

PI WPI; 1997-470545/43.

DR Inhibiting cell proliferation by altering Egr-1 levels - useful in

XX

transcriptional activator
 JOURNAL Mol. Cell. Biol. 10 (7), 3456-3467 (1990)
 MEDLINE 90287135
 PUBMED 2113174
 FEATURES
 source location/Qualifiers
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 /db_xref="taxon:10090"
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 /db_xref="GI:198607"
 /translation="MAAKAKEMOLMSPQLQSDPGSPHSPMDNY"
 BASE COUNT 60 a 170 c 103 g 57 t
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 Query Match 100.0%; Score 15; DB 10; Length 390;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 |||||||
 Db 309 CTTGGCCGCTGCCAT 295
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 LOCUS RNRKRX1 676 bp mRNA linear ROD 27-JUL-2000
 DEFINITION Rattus norvegicus Krox-24 mRNA, partial cds.
 ACCESSION U75398
 VERSION U75398.1 GI:1732257
 KEYWORDS
 SEGMENT 1 of 2
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 676)
 Adams, L.D., Lemire, J.M. and Schwartz, S.M.
 A systematic analysis of 40 random genes in cultured vascular
 smooth muscle subtypes reveals a heterogeneity of gene expression
 and identifies the tight junction gene zonula occludens 2 as a
 marker of epithelioid 'pup' smooth muscle cells and a participant
 in carotid neointimal formation
 Arterioscler. Thromb. Vasc. Biol. 19 (11), 2600-2608 (1999)
 JOURNAL MEDLINE 20027749
 PUBMED 10559001
 REFERENCE 2 (bases 1 to 676)
 AUTHORS Adams, L.A., Merry, I. and Schwartz, S.M.
 TITLE Direct Submision
 JOURNAL Submitted (18-OCT-1996) Pathology, University of Washington, 1959
 NE Pacific, Seattle, WA 98195, USA
 FEATURES
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 1..331
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 332..>676
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 /product="Krox-24"
 /protein_id="AAB38708.1"

/db_xref="GI:1732260"
 /translation="MDNTPKLEEMLLSNGAPDPIGAAGTEPGSGGNNSSSSXXXXG
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 ITTGFRFLSEDPAP"
 BASE COUNT 133 a 258 c 179 g 100 t 6 others.
 ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 676;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 |||||||
 Db 262 CTTGGCCGCTGCCAT 248
 RESULT 3
 LOCUS AR012087/c 843 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 9 from patent US 5763209.
 ACCESSION AR012087
 VERSION AR012087.1 GI:3970077
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 843)
 TITLE Sukhatme, V.P.
 JOURNAL Methods and materials relating to the functional domains of DNA
 binding proteins
 Patent: US 5763209-A 9 09-JUN-1998;
 location/Qualifiers
 1..843
 /organism="unknown"
 BASE COUNT 172 a 299 c 209 g 163 t
 ORIGIN
 Query Match 100.0%; Score 15; DB 6; Length 843;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 |||||||
 Db 15 CTTGGCCGCTGCCAT 1
 RESULT 4
 LOCUS AR014526/c 843 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 9 from patent US 5773583.
 ACCESSION AR014526
 VERSION AR014526.1 GI:3971980
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 843)
 TITLE Sukhatme, V.P.
 JOURNAL Methods and materials relating to the functional domains of DNA
 binding proteins
 Patent: US 5773583-A 9 30-JUN-1998;
 location/Qualifiers
 1..843
 /organism="unknown"
 BASE COUNT 172 a 299 c 209 g 163 t
 ORIGIN
 Query Match 100.0%; Score 15; DB 6; Length 843;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 |||||||

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Db      1 CTTGCCCGCTGCCAT 15
|||||
RESULT 4
AA073457/c
ID      AAF85133 standard; DNA; 15 BP.
XX      AAF85133;
XX      09-JUL-2001 (first entry)
XX      Antisense oligonucleotide which targets an EGR-1 gene.
DE      Antisense oligonucleotide which targets an EGR-1 gene.
XX      Early growth response factor; EGR; tumour cell; tumour; DNase;
XX      antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
XX      skin carcinoma; breast tumour; phosphorothioate; ss.
XX      Synthetic.
XX      Key
XX      Location/Qualifiers
XX      modified_base 1..15
XX      /tag= a
XX      /note= "phosphorothioate-linked bases"
XX      WO200130394-A1.
XX      03-MAY-2001.
XX      26-OCT-2000; 2000WO-AU01315.
XX      26-OCT-1999; 99AU-0003676.
XX      (UNIX ) UNISEARCH LTD.
XX      Khachigian LM;
XX      WPI; 2001-300428/31.
XX      Treating tumors including prostate tumour, breast tumour, skin carcinoma,
XX      comprises administering agent which inhibits induction or decreases
XX      expression of early growth response factor-1
XX      Example 1; Page 24; 80pp; English.
XX      The present sequence represents an antisense oligonucleotide, which
XX      targets an early growth response factor (EGR) gene. The specification
XX      describes a method for inhibiting the growth or proliferation of a tumour
XX      cell and treating tumours. The method comprises contacting a tumour cell
XX      or administering to a subject, an agent which inhibits induction,
XX      decreases expression or which decreases the nuclear accumulation or
XX      activity of EGR. The agent is a DNase or an antisense oligonucleotide.
XX      The method is useful for treating solid tumours, including prostate
XX      tumours, hepatocellular carcinoma, skin carcinoma or breast tumours.
XX      Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 other;
XX
Query Match      100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 CTTGCCCGCTGCCAT 15
|||||
Db      1 CTTGCCCGCTGCCAT 15
|||||
RESULT 5
AA073457/c
ID      AA073457 standard; DNA; 843 BP.
XX      AA073457;
XX      06-MAY-1995 (first entry)

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```

XX      Egr-1 transcription activator domain.
DE      Egr-1 transcription activator domain.
XX      Early growth regulatory protein; Egr-1; zinc finger;
XX      DNA binding protein; cell growth; transcription activator;
XX      nuclear localization; polynucleotide binding; ss.
XX      Mus sp.
XX      WO9423030-A.
XX      13-OCT-1994.
XX      10-MAR-1994; 94WO-US02611.
XX      31-MAR-1993; 93US-0040548.
XX      (ARCH-) ARCH DEV CORP.
XX      Sukhame VP;
XX      WPI; 1994-333191/41.
XX      New early growth regulatory polypeptide and related DNA - useful
XX      for modulating transcription, localisation and binding of
XX      polynucleotide(s)
XX      Disclosure; Page 92; 145pp; English.
XX      Clone OC3.1 was isolated from a cDNA library derived from
XX      BALB/c 3T3 mouse cells, and designated Egr-1. Particular domains of
XX      Egr-1 protein have specific functions: activation of transcription
XX      (domains given in AAR63131-32), repression of transcription
XX      (AAR63133), nuclear localization (AAR63134-35), and polynucleotide
XX      binding (AAR63136). DNA sequences AA073457-62 respectively encode
XX      the peptides given in AAR63131-36. Virus and plasmid vectors
XX      containing such sequences can be used (by transfection or
XX      transformation) to regulate transcription in prokaryotic or
XX      eukaryotic hosts.
XX      Sequence 843 BP; 172 A; 299 C; 209 G; 163 T; 0 other;
XX
Query Match      100.0%; Score 15; DB 15; Length 843;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 CTTGCCCGCTGCCAT 15
|||||
Db      15 CTTGCCCGCTGCCAT 1
|||||
RESULT 6
AA064275/c
ID      AAV64275 standard; DNA; 3068 BP.
XX      AAV64275;
XX      27-JAN-1999 (first entry)
XX      Mouse Egr-1 cDNA.
XX      Egr-1; murine; early growth response protein; inhibitor; tumour; mitogen;
XX      platelet-derived growth factor; PDGF; retroviral vector; osteosarcoma;
XX      zinc finger domain; fibrosarcoma; glioblastoma; carcinoma; ds.
XX      Mus sp.
XX      Key
XX      Location/Qualifiers
XX      CDS 370..1860
XX      /tag= a
XX      /product= "Egr-1"
XX      US5837692-A.

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1. 1983
/organism="Mus musculus"
/db.xref="taxon:10090"
/map="18 bands C-D"
/clone_1lb="cosmid clone 2/2"
1185. 1971
/gene="Krox-24"
/notes="minor transcription start site"
/number=1
protein_bind
1254. 1261
/gene="Krox-24"
/bound_molety="Sp1"
1325. 1330
/gene="Krox-24"
/bound_molety="Sp1"
1366. 1370
/gene="Krox-24"
/bound_molety="AP1"
1395. 1971
/gene="Krox-24"
/notes="major transcription start site"
/number=1
exon
352 a 687 c 630 g 314 t
BASE COUNT
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 1983;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CTTGGCCGCTGCCAT 15
|||||
Db 1688 CTTGGCCGCTGCCAT 1674

RESULT 8
CHKFOA/c
LOCUS 2253 bp mRNA linear VRT 28-APR-1993
DEFINITION Chicken c-fos proto-oncogene mRNA, complete cds.
ACCESSION M37000
VERSION M37000.1 GI:2114169
KEYWORDS c-fos proto-oncogene.
SOURCE Chicken embryo fibroblast, cDNA to mRNA.
ORGANISM Gallus gallus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 2253)
Molders, H., Jenuwein, T., Adamkiewicz, J. and Muller, R.
Isolation and structural analysis of a biologically active chicken
c-fos cDNA: Identification of evolutionarily conserved domains in
fos protein
Oncogene 1 (4), 377-385 (1987)
JOURNAL
MEDLINE 88262231
PUBMED 3330781
FEATURES
source
Location/Qualifiers
1..2253
/organism="Gallus gallus"
/db.xref="taxon:9031"
125. 1228
/notes="c-fos proto-oncogene product"
/codon_start=1
/protein_id="AA048670.1"
/db_xref="GI:211470"
/translat="MMTQFAGEYAEAPSSRCSSASPAAGSLITYPSPADSSGSGSPV
NSQDFCTDLAVSSANFPTVTAISTPDLMVOPITISSVASQNGHYGAPAP
PAAYSRPAVAKAGRGOSIGRGKYVLSPEEERKRIIRERKMAACRRRRRL
TDLQATPDLEEKSALEINILKEKLEPILAAHSPACKMPPELAFSEELAA
TALDLGAPPAALAEAFALPMTEAPAYVPRKSGSGELKAPPELIPSKPREA
SRSPVMDLPCASSFYASDMPEIGAGSGGELPCTPVYTCPTCPSTYSTVFVTYPE
ADAFPCAAAHRRGSSSENESDLSLSPFLAL"
BASE COUNT 399 a 729 c 647 g 478 t
ORIGIN

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Query Match
Best Local Similarity 100.0%; Score 15; DB 5; Length 2253;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CTTGGCCGCTGCCAT 15
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Db 580 CTTGGCCGCTGCCAT 566

RESULT 9
GDFOS/c
LOCUS 2253 bp mRNA linear VRT 02-APR-1988
DEFINITION Chicken fos proto-oncogene mRNA.
ACCESSION Y00659
VERSION Y00659.1 GI:62891
KEYWORDS fos cellular oncogene; proto-oncogene.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 2253)
Molders, H.
Direct Submission
Submitted (18-NOV-1987) Molders H., EMBL, Postfach 10.2209, D-6900
Heidelberg, West-Germany
2 (bases 1 to 2253)
Molders, H., Jenuwein, T., Adamkiewicz, J. and Muller, R.
Isolation and structural analysis of a biologically active chicken
c-fos cDNA: Identification of evolutionarily conserved domains in
fos protein
Oncogene (1987) In press
JOURNAL
FEATURES
source
Location/Qualifiers
1..2253
/organism="Gallus gallus"
/strain="SPAFAS"
/db.xref="taxon:9031"
/codon_start=1
/clone_1lb="pex 1"
125. 1225
/notes="fos-protein"
misc_feature
399 a 729 c 647 g 478 t
BASE COUNT
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 15; DB 5; Length 2253;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CTTGGCCGCTGCCAT 15
|||||
Db 580 CTTGGCCGCTGCCAT 566

RESULT 10
DVHRYWNGA
LOCUS 2700 bp mRNA linear INV 24-NOV-1993
DEFINITION D.virilis Hairy-wing protein mRNA, complete cds.
ACCESSION 225520
VERSION 225520.1 GI:396676
KEYWORDS Hairy-wing protein.
SOURCE Drosophila virilis.
ORGANISM Drosophila virilis
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2700)
Corces, V.G.
Direct Submission
Submitted (01-JUL-1993) Corces V. G., The Johns Hopkins University,
Biology, 34th and Charles Sts, Baltimore, Maryland, USA, 21218
2 (bases 1 to 2700)
Harrison, D.A., Gdula, D.A., Coyne, R.S. and Corces, V.G.
A leucine zipper domain of the suppressor of Hairy-wing protein

```


BASE COUNT 706 a 939 c 705 g 736 t
 ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 3086;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCCCGCTGCCAT 15
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 DB 273 CTTGCCCGCTGCCAT 259

|||||||||||||
 DB 283 CTTGCCCGCTGCCAT 269

Search completed: December 16, 2002, 13:34:52
 Job time : 3187 secs

RESULT 14

AR014532/c AR014532 3086 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 15 from patent US 5773583.
 ACCSSION AR014532
 VERSION AR014532.1 GI:3971986
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3086)
 AUTHORS Sukhatme,V.P.

TITLE Methods and materials relating to the functional domains of DNA
 binding proteins

JOURNAL Patent: US 5773583-A 15 30-JUN-1998;

FEATURES
 Location/Qualifiers
 1..3086
 /organism="unknown"

BASE COUNT 706 a 939 c 705 g 736 t
 ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 3086;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCCCGCTGCCAT 15
 |||||||||||||||
 DB 273 CTTGCCCGCTGCCAT 259

RESULT 15

AX401867/c AX401867 3112 bp DNA linear PAT 06-JUN-2002
 DEFINITION Sequence 1543 from Patent W00210453.
 ACCSSION AX401867
 VERSION AX401867.1 GI:21338047
 KEYWORDS

SOURCE Norway rat.
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1
 AUTHORS Mendlick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and
 Elashoff,M.R.

TITLE Molecular toxicology modeling
 JOURNAL Patent: WO 0210453-A 1543 07-FEB-2002;

FEATURES
 Location/Qualifiers
 1..3112
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /note="EMBL/GenBank Accession No. NM_012551"

BASE COUNT 708 a 951 c 711 g 742 t
 ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 3112;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCCCGCTGCCAT 15

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/clone="whyf13f09"
/clone_lib="y" Oglhara unpublished cDNA library, whyf
/tissue_type="spikelet at early flowering"
/dev_stage="feekes" scale 6
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give Bluescript phagemids in the TI Close Lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhan).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson Lab (all other authors)."
```

BASE COUNT 74 a 58 c 68 g 50 t 5 others

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 255;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCCCGCTGCCAT 15
|||||

DB 208 CTTGCCCGCTGCCAT 194

RESULT 2
BE204615/c 364 bp mRNA linear EST 05-SEP-2000

LOCUS BE204615

DEFINITION EST397291 KVO Medicago truncatula cDNA clone PKV0-1606, mRNA

ACCESSION BE204615

VERSION BE204615.1 GI:8747903

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

REFERENCE 1 (bases 1 to 364)
Vandenbosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
ESTs from uninoculated seedling roots of Medicago truncatula
Unpublished (1999)

JOURNAL Contact: Vandenbosch K

COMMENT Department of Plant Biology
University of Minnesota
220 Bloss Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenbosch@umn.edu
Texas A&M University name: T264387e
TIGR sequence name: MTGAX517K
More information is available at:
http://chrysl.tamu.edu/medicago
Seq primer: SKmod (CTA GAA CTA gty gat CC).

FEATURES

source

1..364
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="PKV0-1606"
/clone_lib="KV0"
/tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E.coli strain XL0LR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

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XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the unizap XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-Assist
helper phage and propagated in XL0LR cells."
```

BASE COUNT 108 a 64 c 92 g 100 t

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 364;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCCCGCTGCCAT 15
|||||

DB 275 CTTGCCCGCTGCCAT 261

RESULT 3
BF518720/c 370 bp mRNA linear EST 08-DEC-2000

LOCUS BF518720

DEFINITION EST456171 DSIL Medicago truncatula cDNA clone pDSIL-17D11, mRNA

ACCESSION BF518720

VERSION BF518720.1 GI:11607403

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

REFERENCE 1 (bases 1 to 370)
Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng
H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
Holt,I.E. and Fraser,C.M.
ESTs from leaves of Medicago truncatula after inoculation with
Colletotrichum trifolii
Unpublished (2000)

JOURNAL Contact: Deborah A. Samac

COMMENT Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@pnucn1.crl.umn.edu
University of Minnesota name: M276140e
TIGR sequence name: MTBPU18TK
More information is available at: http://chrysl.tamu.edu/medicago
Seq primer: SKmod (CTA GAA CTA gty gat CC).

FEATURES

source

1..370
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSIL-17D11"
/clone_lib="DSIL"
/tissue_type="leaves infected with Colletotrichum
trifolii"

/dev_stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifolii. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-Assist
helper phage and propagated in XL0LR cells. Note: EST may
be of fungal origin."

BASE COUNT 106 a 67 c 96 g 100 t 1 others

ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 370;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||

DB 275 CTTGGCCGCTGCCAT 261

RESULT 4
 AJ503983/c 380 bp mRNA linear EST 09-AUG-2002
 LOCUS AJ503983 MTAMP Medicago truncatula cDNA clone mtgmadc120040g11,
 DEFINITION mRNA sequence.
 AJ503983
 VERSION AJ503983.1 GI:22084911
 KEYWORDS EST.
 SOURCE batrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 380)
 Mantley,K., Bartelsmeier,V., Baler,M.C., Meyer,F., Bartels,D.,
 Bekei,T., Linke,B., Grunwald,U., Franken,P., Kuester,H., Perlick
 ,A.M. and Puehler,A.
 TITLE Detection of transcript sequences from mycorrhizal roots of the
 model mycorrhiza Medicago truncatula genotype A17 - Glomus mosseae
 using the approach of an EST genome project
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kuester H
 Lehrstuhl fuer Genetik
 Universitaet Bielefeld
 Postfach 100131, D-33501 Bielefeld, Germany.
 FEATURES Location/Qualifiers
 source 1..380
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="mtgmadc120040g11"
 /clone_1lb="MTAMP"
 /tissue_type="mycorrhizal roots"
 /dev_stage="three weeks"
 /note="Vector: pGEM-T; Site 1: PstI; Site 2: SphI;
 genotype A17; cDNA was prepared from polyA+ enriched RNA
 from mycorrhizal roots harvested after three weeks. The
 cDNA was directionally ligated by Medigenomix into the
 pGEM-T vector from Promega using GCATGCCGCCGAGCGCGCATG
 and CTCGAGCGCATATGCGCGG adapters. Plasmids containing
 cDNA inserts were propagated in E. coli DH10B cells."

BASE COUNT 108 a 73 c 97 g 100 t 2 others

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||

DB 302 CTTGGCCGCTGCCAT 288

RESULT 5
 BF116561/c 386 bp mRNA linear EST 29-DEC-2000
 LOCUS BF116561 u90f01.y1 NCI-CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666841 5',
 DEFINITION similar to SW:EGRL_MOUSE P08046 EARLY GROWTH RESPONSE PROTEIN 1,;
 mRNA sequence.
 BF116561
 VERSION BF116561.1 GI:10986037
 KEYWORDS EST.

SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 386)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
image.llnl.gov/image/html/lresources.shtml

MG1:1427609
 Seq primer: -40RP from Gibco
 High quality sequence stop: 355.
 Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:3666841"
 /clone_1lb="NCI-CGAP_Mam5"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: oligo dt.
 library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 61 a 161 c 104 g 60 t

ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 386;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||

DB 265 CTTGGCCGCTGCCAT 251

RESULT 6
 AN209329/c 404 bp mRNA linear EST 03-DEC-1999
 LOCUS u007f01.y1 NCI-CGAP_Mam6 Mus musculus cDNA clone IMAGE:2598841 5',
 DEFINITION similar to gb:M62829 EARLY GROWTH RESPONSE PROTEIN 1 (HUMAN);
 gb:M22326 Mouse growth factor-induced protein (MOUSE);, mRNA
 sequence.
 AN209329
 VERSION AN209329.1 GI:6515344
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 404)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.


```

XX 17-NOV-1998.
PD
XX 07-APR-1994; 94US-0224482.
XX 07-APR-1994; 94US-0224482.
XX 07-APR-1994; 94US-0224482.
XX (ADAM/) ADAMSON E.
XX (MERC/) MERCOLA D.
XX
XX Adamson E, Mercola D;
XX
XX WPI: 1999-023510/02.
XX P-PSDB: AAW76984.
XX
XX Inhibiting the growth of tumours - using a vector encoding a
XX mammalian early growth response polypeptide or fragment to inhibit
XX the mitogenic activity of platelet-derived growth factor
XX
XX Disclosure; Fig 2A; 40pp; English.
XX
XX This sequence encodes a mouse early growth response protein, Egr-1 which
XX is used in a method to inhibit the growth of a tumour in a mammal where
XX the growth is induced by the mitogenic activity of platelet-derived
XX growth factor, PDGF. The method involves directly administering to the
XX tumour a retroviral vector comprising an expression control sequence
XX operatively linked to a nucleic acid sequence encoding a mammalian Egr-1
XX polypeptide, a nucleic acid sequence encoding a fragment of a mammalian
XX Egr-1 polypeptide comprising the zinc finger domain or a nucleic acid
XX sequence that both hybridises to any of the described nucleic acid
XX sequences, under standard hybridisation conditions, and also encodes a
XX polypeptide that inhibits the mitogenic activity of PDGF. The methods can
XX be used for inhibiting the growth of a tumour such as an osteosarcoma, a
XX fibrosarcoma, a glioblastoma, or a breast carcinoma.
XX
SQ Sequence 3068 BP; 688 A; 939 C; 705 G; 736 T; 0 other;
Query Match 100.0%; Score 15; DB 20; Length 3068;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTGGCCCGCTGCCAT 15
DB 273 CTGGCCCGCTGCCAT 259

```

```

PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.
XX
XX Atkins DG, Baker AR, Khachigian LM;
XX
XX WPI: 2000-476054/41.
XX
XX DNAzyme for treating conditions associated with proliferation or
XX migration of cells e.g. post-angioplasty restenosis, vein graft failure
XX and hypertension cleaves mRNA molecules encoding EGR-1
XX
XX Disclosure; Pages 14-21; 62pp; English.
XX
XX The present sequence is mouse Egr-1 (also known as NGFI-A and EGR-1).
XX Egr-1 is a transcription factor. Egr-1 binds to the promoters of genes
XX whose products influence cell movement and replication in the artery
XX wall. DNA-based enzymes (DNAzymes), have been developed in the present
XX invention (see AAF74387-A74394), which can cut Egr-1 mRNA with high
XX efficiency and specificity, resulting in Egr-1 activity inhibition in
XX vascular smooth muscle cells. The DNAzymes of the present invention can
XX be used to inhibit EGR-1 activity in cells, inhibit proliferation or
XX migration of cells and to treat a condition associated with cell
XX proliferation or migration e.g. post-angioplasty restenosis, vein graft
XX failure, transplant coronary disease and complications associated with
XX atherosclerosis e.g. cerebrovascular infarction (stroke), myocardial
XX infarction (heart attack), hypertension or peripheral vascular disease
XX e.g. gangrene of the extremities. The cells which are treated are
XX vascular cells, preferably smooth muscle or endothelial cells or cells
XX involved in neoplasia.
XX
SQ Sequence 3068 BP; 688 A; 939 C; 705 G; 736 T; 0 other;
Query Match 100.0%; Score 15; DB 21; Length 3068;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTGGCCCGCTGCCAT 15
DB 273 CTGGCCCGCTGCCAT 259

```

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RESULT 7
AAAF4395/c
ID AAA74395 standard; CDNA: 3068 BP.
XX
XX AAA74395;
AC
XX 30-NOV-2000 (first entry)
DT
XX
XX Mouse Egr-1 coding sequence.
DE
XX
XX Mouse; Egr-1; NGFI-A; transcription factor; DNazyme;
XX vascular smooth muscle cell; post-angioplasty restenosis;
XX vein graft failure; transplant coronary disease; atherosclerosis;
XX cerebrovascular infarction; stroke; myocardial; heart attack;
XX hypertension; peripheral vascular; gangrene; neoplasia; ss.
XX
XX Mus sp.
OS
XX
XX WO200042173-A1.
XX
XX 20-JUL-2000.
XX
XX 11-JAN-2000; 2000WO-AU00011.
XX
XX 11-JAN-1999; 99AU-0008103.
XX
XX (UNIX) UNISEARCH LTD.
PA

```

```

RESULT 8
AAF85130/c
ID AAF85130 standard; DNA: 3068 BP.
XX
XX AAF85130;
AC
XX 09-JUL-2001 (first entry)
DT
XX
XX Nucleotide sequence of murine early growth response factor-1.
DE
XX
XX Early growth response factor; EGR; tumour cell; tumour; DNazyme;
XX antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
XX skin carcinoma; breast tumour; ss.
XX
XX Mus musculus.
OS
XX
XX WO200130394-A1.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-AU01315.
XX
XX 26-OCT-1999; 99AU-0003676.
XX
XX (UNIX) UNISEARCH LTD.
XX
XX Khachigian LM;
XX
XX WPI: 2001-300428/31.
XX
XX Treating tumors including prostate tumour, breast tumour, skin carcinoma,
XX comprises administering agent which inhibits induction or decreases
XX expression of early growth response factor-1
XX

```

mediates its repressive effect on enhancer function
 Genes Dev. 7 (10), 1966-1978 (1993)

JOURNAL
 MEDLINE
 PUBMED
 FEATURES

source

Location/Qualifiers
 1.2700

ORGANISM="Drosophila virilis"
 /db_xref="taxon:7244"
 1.2700

CDS

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 ADDEVELGAKENGEFVSVGDEDDDDDEDEGVEGKRRSGNNLEKVEH
 VCGKCTKTRRVKSLKHLKLEFCRYDSGYHLKRAMDKLNEKIDAVNEKDISCC
 SESYDFHLGHINCPCPKSPKTSYERHIFTHSWSNDYPCISGNALSGALK
 LHEOQHLRGKFPACKICGKDEPCSYHLCHOKYSSCSANENDMCKCDRFEYLD
 NCALHKLHGLTOVYKPKPEYHVCNCFYSSTLNHTRHTEGKPEPCDLCDKES
 ALVALKKHRRYHREKPYCTCYSCSFAYKLYLNRMKHTSERPKNCEKCSFIOA
 TOLRTHSKTHLRPACSLIQKFKTEKOLRHYKDHTRKRAFSFACTECTSRISAL
 LKHEHDAGHSPVSKTRAKRSAMIERTCADKNDFTETLRNHRVHEDDPDI
 FGTEPPAKRKARKTYVAVAEIOKEQEDVPAKNISAKISKTGDNVAVVEEFLD
 EGDNGAKITDLKRGHLHLPLEQDKATESTAEIDIAESSEKSPVVKKEQKSL
 AASIAAIADNLEESDEFSGEVLEEDLAKENIATIDMLVDPOLTKKYGPN
 SSESVCYKYEKGHDLAKSEAVYELDYGSRMPTIOLFTFYVYIHDSIKALLNPI
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BASE COUNT
 ORIGIN

743 a 705 c 764 g 488 t

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QY 1 CTTGGCCGCTGCCAT 15

Db 2229 CTTGGCCGCTGCCAT 2243

RESULT 11
 ARO58196/c

LOCUS ARO58196 3068 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 1 from patent US 5837692.
 ACCESSION ARO58196
 VERSION ARO58196.1 GI:5983773

KEYWORDS

SOURCE
 ORGANISM

REFERENCE
 1 (bases 1 to 3068)

AUTHORS Mercola,D. and Adamson,E.
 TITLE Inhibition of the mitogenic activity of PDGF by mammalian Egr
 JOURNAL Patent: US 5837692-A 1 17-NOV-1998;
 FEATURES Location/Qualifiers
 1.3068

BASE COUNT 688 a 939 c 705 g 736 t
 ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 15; DB 6; Length 3068;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15

Db 273 CTTGGCCGCTGCCAT 259

RESULT 12

MUSEGRIA/c
 LOCUS MUSEGRIA 3068 bp mRNA linear ROD 12-JUN-1993
 DEFINITION Mouse Egr-1 mRNA, complete cds.
 ACCESSION M20157
 VERSION M20157.1 GI:193009
 KEYWORDS Egr-1 gene.
 SOURCE Mouse (strain BALB/c) fibroblast, cDNA to mRNA, clones OC68, OC19c, and OC3.1.
 ORGANISM Mus musculus

REFERENCE
 1 (bases 1 to 3068)
 Sukhatme,V.P., Cao,X., Chang,L.C., Tsai-Morris,C.-H.,
 Stamenkovic,I.D., Ferreira,P.C.P., Cohen,D.R., Edwards,S.A.,
 Shows,T.B., Jr., Curran,T., Le Beau,M.M. and Adams,J.E.D.
 A zinc finger-encoding gene co-regulated with c-fos during growth
 and differentiation, and after cellular depolarization

JOURNAL Cell 53 (1), 37-43 (1988)
 MEDLINE 88165055
 PUBMED 3127059

COMMENTARY
 Draft entry and computer-readable sequence [1] kindly submitted by
 V.P. Sukhatme 15-NOV-1988.

FEATURES
 source

mRNA

CDS

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 MNPPTSSSSAPSPASSSSSASQSPPLSCAVPSNDSPIYSAAPFPPTNTDIFPP
 QSGAFPGSAGTALQVPPAYPATKGFQVMPIDYLFPOQGGDLSLGTPOKPFQGLE
 NRTQCSLTPPLSTIKAFATGSGDILKALNTYOSOLIKSRMKYRNRSKTPHER
 PYACPVSQDRRSRSDDELTRHRIHITGOKPQRCICMRNFSDDHTLRHTGCK
 PPAQDLCGRKFRASDERKRTKHLKRODKAKKASYASASLSSTPPVATSYPS
 PATTSFSPVPTSYSSPGSSPTSPSPASGSPSVATFASVPAPFPTQVSSPFSAGV
 SSSFTSTGSLDMTATSPETIDIC"

BASE COUNT
 ORIGIN

688 a 939 c 705 g 736 t

Query Match
 Best Local Similarity 100.0%; Score 15; DB 10; Length 3068;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15

Db 273 CTTGGCCGCTGCCAT 259

RESULT 13
 ARO12093/c

LOCUS ARO12093 3066 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 15 from patent US 5763209.
 ACCESSION ARO12093
 VERSION ARO12093.1 GI:3970083

KEYWORDS

SOURCE
 ORGANISM

REFERENCE
 1 (bases 1 to 3066)

AUTHORS Sukhatme,V.P.
 TITLE Methods and materials relating to the functional domains of DNA
 binding proteins
 JOURNAL Patent: US 5763209-A 15 09-JUN-1998;
 FEATURES Location/Qualifiers
 1.3066
 /organism="unknown"

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTTGCCCGCTGCCAT 15
 Db 273 CTTGCCCGCTGCCAT 259

RESULT 11
 ABR63636/C

ID ABR63636 standard; cDNA; 3112 BP.

AC ABR63636;

DT 18-JUN-2002 (first entry)

DE Rat sequence differentially expressed in response to a hepatotoxin #1543.

KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 KM differential expression; centrilobular necrosis; steatosis.

OS Rattus norvegicus.

PN WO200210453-A2.

PD 07-FEB-2002.

PF 30-JUL-2001; 2001WO-US33872.

PR 31-JUL-2000; 2000US-222040P.

PR 02-NOV-2000; 2000US-244880P.

PR 11-MAY-2001; 2001US-290023P.

PR 15-MAY-2001; 2001US-290645P.

PR 22-MAY-2001; 2001US-292336P.

PR 06-JUN-2001; 2001US-295798P.

PR 13-JUN-2001; 2001US-297457P.

PR 19-JUN-2001; 2001US-298884P.

PR 09-JUL-2001; 2001US-303459P.

XX (GENE-) GENE LOGIC INC.

PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;

XX WPI: 2002-241625/29.

Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells -

Claim 1; Seq ID No 1543; 239pp; English.

The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilize a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in

tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent.

Sequence 3112 BP; 708 A; 951 C; 711 G; 742 T; 0 other.

Query Match 100.0%; Score 15; DB 24; Length 3112;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTTGCCCGCTGCCAT 15

Db 283 CTTGCCCGCTGCCAT 269

RESULT 12

ID AAA74396 standard; cDNA; 4321 BP.

AC AAA74396;

DT 30-NOV-2000 (first entry)

DE Rat Egr-1 coding sequence.

KW Rat; Egr-1; NGF1-A; transcription factor; DNazyme;

KW vascular smooth muscle cell; post-angioplasty restenosis;

KW vein graft failure; transplant coronary disease; atherosclerosis;

KW cerebrovascular infarction; stroke; myocardial; heart attack;

KW hypertension; peripheral vascular; gangrene; neoplasia; ss.

OS Rattus sp.

PN WO200042173-A1.

PD 20-JUL-2000.

PF 11-JAN-2000; 2000WO-A000011.

PR 11-JAN-1999; 99AU-0008103.

XX (UNITX) UNISEARCH LTD.

PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.

PI Atkins DG, Baker AR, Khachigian LM;

XX WPI: 2000-476054/41.

DNazyme for treating conditions associated with proliferation or migration of cells, e.g. post-angioplasty restenosis, vein graft failure and hypertension cleaves mRNA molecules encoding EGR-1 -

Disclosure: Pages 14-21; 62pp; English.

The present sequence is rat Egr-1 (also known as NGF1-A and EGR-1). Egr-1 is a transcription factor. Egr-1 binds to the promoters of genes whose products influence cell movement and replication in the artery wall. DNA-based enzymes (DNazymes), have been developed in the present invention (see AAA74387-A74394), which can cut Egr-1 mRNA with high efficiency and specificity, resulting in Egr-1 activity inhibition in vascular smooth muscle cells. The DNazymes of the present invention can be used to inhibit EGR-1 activity in cells, inhibit proliferation or migration of cells and to treat a condition associated with cell proliferation or migration e.g. post-angioplasty restenosis, vein graft failure, transplant coronary disease and complications associated with atherosclerosis e.g. cerebrovascular infarction (stroke), myocardial infarction (heart attack), hypertension or peripheral vascular disease e.g. gangrene of the extremities. The cells which are treated are

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 11:13:08 ; Search time 3183 Seconds

(without alignments)
137.148 Million cell updates/sec

Title: US-09-648-389A-1

Perfect score: 15

Sequence: 1 cttgcgcgcgcgcac 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: gb_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pin:*
35: em_hg_rod:*
36: em_hg_mam:*
37: em_hg_vrt:*
38: em_sy:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	100.0	390	10	MUSKROX24A	M38174 Mouse nucle
2	15	100.0	676	10	RNKR0X1	U75398 Rattus norv
3	15	100.0	843	6	AR012087	AR012087 Sequence
4	15	100.0	843	6	AR014526	AR014526 Sequence
5	15	100.0	933	8	CAR6024	AJ006024 Cicer ari
6	15	100.0	1980	14	AC2NKR24	M18041 Avian trans
7	15	100.0	1983	10	MUSKROX251	M28844 Mus musculu
8	15	100.0	2253	5	CHKCFOSA	M37000 Chicken c-f
9	15	100.0	2253	5	GDPOS	Y00659 Chicken fos
10	15	100.0	2700	3	DVHRYNMGA	225520 D.villilis H
11	15	100.0	3068	6	AR058196	AR058196 Sequence
12	15	100.0	3068	10	MUSEGR1A	M20157 Mouse Egr-1
13	15	100.0	3086	6	AR012093	AR012093 Sequence
14	15	100.0	3086	6	AR014532	AR014532 Sequence
15	15	100.0	3112	6	AX401867	AX401867 Sequence
16	15	100.0	3112	10	RATNGFLA	M18416 Rat nerve g
17	15	100.0	3858	5	CHKCFOS	M18043 Chicken c-f
18	15	100.0	4321	10	RATNGFLA	J04154 Rattus norv
19	15	100.0	4494	6	AX306251	AX306251 Sequence
20	15	100.0	4494	10	MUSTPEZIF	M22326 Mouse growt
21	15	100.0	10528	1	AE009847	AE009847 Pyrodacul
22	15	100.0	38343	3	CEP21D9	281510 Caenorhabdi
23	15	100.0	56870	2	CEY39B6_3	Continuation (4 of
24	15	100.0	59907	2	AC130689	AC130689 Homo sapi
25	15	100.0	71503	2	AC129488	AC129488 Homo sapi
26	15	100.0	71503	2	AC129488	AC129488 Homo sapi
27	15	100.0	127304	2	AC119051	AC119051 Gallus ga
28	15	100.0	140053	2	AC007873	AC007873 Homo sapi
29	15	100.0	153695	2	CNS08CAL	AL831808 Oryza sat
30	15	100.0	153824	2	AC118806	AC118806 Rattus no
31	15	100.0	166138	2	AC099684	AC099684 Homo sapi
32	15	100.0	175131	2	AC114820	AC114820 Mus muscu
33	15	100.0	190875	2	AC022255	AC022255 Homo sapi
34	15	100.0	208395	2	AC098450	AC098450 Rattus no
35	15	100.0	212696	2	AL772410	AL772410 Mus muscu
36	15	100.0	212696	2	AL772410	X88786 Porcine viru
37	14	93.3	708	14	PVXCPWS2	M34453 S.mansoni 2
38	14	93.3	1058	38	SCMIMP23A	BC022626 Mus muscu
39	14	93.3	1434	10	BC022626	X57478 S.cerevisia
40	14	93.3	1606	9	SCMTR1	AL833144 Homo sapi
41	14	93.3	1873	9	HSMB04455	AF176328 Mus muscu
42	14	93.3	1922	10	AF176328	BC010694 Mus muscu
43	14	93.3	1938	10	BC010694	217317 Kluyveromyc
44	14	93.3	1961	9	KLTRANAL6	BC029146 Homo sapi
45	14	93.3	2100	6	AX121824	AX121824 Sequence

ALIGNMENTS

RESULT 1
MUSKROX24A/c 390 bp mRNA linear ROD 27-Apr-1993
LOCUS MUSKROX24A
DEFINITION Mouse nuclear protein Krox-24 mRNA, 5' end.
ACCESSION M38174
VERSION M38174.1 GI:198606
KEYWORDS nuclear protein; transcriptional activator.
SOURCE Mouse, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 390)
AUTHORS Lemaire,P., Vesque,C., Schmitt,J., Stunnenberg,H., Frank,R. and
Charney,P.
TITLE The serum-inducible mouse gene Krox-24 encodes a sequence-specific

Db 15 CTTGGCCGCTGCCAT 1

RESULT 5
LOCUS CAR6024/c 953 bp mRNA linear PLN 11-MAY-1998

DEFINITION Cicer arletinum mRNA for cysteine synthase, partial.

ACCESSION AJ006024

VERSION AJ006024.1 GI:3127889

KEYWORDS cysteine synthase.

SOURCE chickpea.

ORGANISM Cicer arletinum

REFERENCE 1 (bases 1 to 953)
AUTHORS Labrador, E.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-1998) Labrador E., Dpto. Fisiologia Vegetal, Univ. Salamanca, Campus Miguel de Unamuno. Pza. Doctores de la Reina s/n, 37007-Salamanca, SPAIN

REFERENCE 2 (bases 1 to 953)
AUTHORS Dopico, B., Esteban, R. and Labrador, E.
TITLE CDNA expressed in chickpea epicotyls
JOURNAL Unpublished

FEATURES
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BASE COUNT 288 a 169 c 229 g 267 t

ORIGIN

Query Match 100.0%; Score 15; DB 8; Length 953;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
|||||

Db 101 CTTGGCCGCTGCCAT 87

RESULT 6
LOCUS AC2NK24 1980 bp ss-RNA linear VRL 10-MAY-1995

DEFINITION Avian transforming proviral retrovirus NK24 v-fos gene, partial cds.

ACCESSION M18041

VERSION M18041.1 GI:209654

KEYWORDS c-myc proto-oncogene; fos gene.

SOURCE Avian transforming proviral retrovirus NK24 RNA, from a chicken nephroblastoma, passed in quail embryo fibroblast (QEF) cells, clone 2401.

ORGANISM Avian carcinoma virus

REFERENCE 1 (bases 1 to 1980)
Virus: Retroviral viruses; Retroviridae; Alpharetrovirus.

AUTHORS Nishizawa, M., Goto, N. and Kawai, S.

TITLE An avian transforming retrovirus isolated from a nephroblastoma that carries the fos gene as the oncogene

JOURNAL J. Virol. 61 (12), 3733-3740 (1987)

MEDLINE 88062920

PUBMED 2824811

COMMENT Printed copy of sequence for [1] kindly provided by S.Kawai, 15-MAR-1988.

FEATURES
source Location/Qualifiers
1..1980
/organism="Avian carcinoma virus"
/db_xref="taxon:11958"
<1..1098
/codon_start=1
/product="gag/NK24 fusion protein"
/protein_id="AAA66158.1"
/db_xref="GI:209655"
/translation="SDLSPTARAPVITDFCRKSPDIOQLRAAPSTLTTCETIINS QDFCTDLAVSSANFVPTVTAISTPDLQVOTLISSVAPSONGHPYGPAPAPA AYSRAVLAKAPGKGQSIGRRGVQLSPSEERKRIIRERNKMAAKRNRRELT DLOAETDLEERKSAIOAEIANLKEKEKLEILAAHRPACMKPELRFSEELAATA LDIGAPSPAAAEAPALPMTAPAPVPPKPEPGSGGLKAPPELLEFAGPREASR SVPMDDLPGASSFVASDMPPELPGAGSGGELEPCTPVVCTPCTPCTPTFTFTTEAD APTSCAAHRRKSSNPSDSLSPTLIAL"

CDS
misc_recomb 128..129
/organism="Avian carcinoma virus"
misc_recomb 1200..1201
/organism="Avian carcinoma virus"
misc_recomb 1255..1256
/organism="Avian carcinoma virus"
1718..>1980
/note="The first start codon in the ORF is located at position 1718; putative"
/codon_start=1
/product="glycoprotein 85"
/protein_id="AAA66159.1"
/db_xref="GI:806277"
/translation="WMDEPDLQLGSOSLPNITNTVQIPVAGGCTGFTPGSPAGV YGMGRGELTHILTNPDNPNFNRASNSTEPTVTYADRHNLF"

BASE COUNT 380 a 667 c 573 g 360 t

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 1980;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
|||||

Db 450 CTTGGCCGCTGCCAT 436

RESULT 7
LOCUS MUSKROX2S1 1983 bp DNA linear ROD 21-MAY-1996

DEFINITION Mus musculus zinc finger protein (Krox-24) gene, exon 1.

ACCESSION M28844

VERSION M28844.1 GI:342026

KEYWORDS DNA-binding protein; zinc finger protein.

SEGMENT 1 of 2

SOURCE Mus musculus DNA.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1983)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Janssen-Timmen, U., Lemaire, P., Matzel, M.G., Revelant, O. and Charney, P.

TITLE Structure, chromosome mapping and regulation of the mouse zinc-finger gene Krox-24: evidence for a common regulatory pathway for immediate-early serum-response genes

JOURNAL Gene 80 (2), 325-336 (1989)

MEDLINE 90060781

PUBMED 2511075

FEATURES
Location/Qualifiers

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1. 409
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBA57D03"
/clone_lib="MCBA"
/tissue_type="root tips"
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ACCESSION AM207985
 VERSION AM207985.2 GI:7773205
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 REFERENCE 1 (bases 1 to 429)
 AUTHORS Fedorova,M., Pletson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P.,
 Gonzales,M.B. and Ellis,L.
 TITLE ESTs from Medicago truncatula roots infected with Phytophthora
 medicaginis
 JOURNAL Unpublished (2000)
 COMMENT On Dec 2, 1999 this sequence version replaced gi:6507422.
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
 Tel: 612 625 5715
 Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 Date: 9/28/99; Updated to the Database of Expressed Sequence Tags
 (dbEST) on 04/27/00; More information is available at
 'http://chryste.tamu.edu/medicago'.
 Seq primer: r3.
 FEATURES
 source
 location/Qualifiers
 1..429
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"
 /clone="r388"
 /clone_lib="DSLR"
 /tissue_type="roots infected with Phytophthora
 medicaginis"
 /dev_stage="roots harvested at 10 days post inoculation
 with Phytophthora medicaginis"
 /lab_host="E. coli strain XLOLR"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA from
 roots harvested at 10 days post inoculation with
 Phytophthora medicaginis. The cDNA was directionally
 ligated into the uni-zap XR vector from Stratagene and
 packaged using GigaPack III Gold packaging extracts.
 Plasmids containing cDNA inserts were excised from the
 recombinant lambda-ZAP phage using Ex-Assist helper phage
 and propagated in XLOLR cells. Note: EST may be of fungal
 origin."
 BASE COUNT 126 a 82 c 105 g 116 t
 ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 429;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 ||||||||||||||||
 Db 350 CTTGGCCGCTGCCAT 336
 RESULT 12
 AM127154/c 438 bp mRNA linear EST 07-SEP-2000
 LOCUS
 DEFINITION M110088 GVN Medicago truncatula cDNA clone N10, mRNA sequence.
 ACCESSION AM127154
 VERSION AM127154.2 GI:7771071
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

Medicago.
 REFERENCE 1 (bases 1 to 438)
 AUTHORS Fedorova,M., Pletson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P.,
 Gonzales,M.B. and Ellis,L.
 TITLE ESTs from effective root nodules of Medicago truncatula
 JOURNAL Unpublished (2000)
 COMMENT On Oct 25, 1999 this sequence version replaced gi:6115058.
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
 Tel: 612 625 5715
 Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 Date: 9/8/99; Updated to the Database of Expressed Sequence Tags
 (dbEST) on 04/27/00; More information is available at
 'http://chryste.tamu.edu/medicago'.
 Seq primer: r3.
 FEATURES
 source
 location/Qualifiers
 1..438
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"
 /clone="N10"
 /clone_lib="GVN"
 /tissue_type="N2-fixing root nodules"
 /dev_stage="effective root nodules harvested one month
 post inoculation with Sinorhizobium meliloti"
 /lab_host="E. coli strain XLOLR"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA from
 effective root nodules harvested one month post
 inoculation with Sinorhizobium meliloti. The cDNA was
 directionally ligated into the Uni-ZAP XR vector from
 Stratagene and packaged using GigaPack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-ZAP phage using Ex-Assist
 helper phage and propagated in XLOLR cells."
 BASE COUNT 136 a 87 c 112 g 103 t
 ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 438;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 ||||||||||||||||
 Db 117 CTTGGCCGCTGCCAT 103
 RESULT 13
 AM321427/c 443 bp mRNA linear EST 25-JAN-2000
 LOCUS
 DEFINITION uc031f11.y1 NCI-CGAP Mamme Mus musculus cDNA clone IMAGE:2631117 5
 similar to gb:M20157 Mouse Egr-1 mRNA, complete cds (MOUSE);, mRNA
 sequence.
 ACCESSION AM321427
 VERSION AM321427.1 GI:6750971
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 443)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 11:13:18 ; Search time 2423 Seconds

(Without alignments)
100.261 Million cell updates/sec

Title: US-09-648-389A-1

Perfect score: 15

Sequence: 1 cttgcccgcgtgccat 15

Scoring table: IDENTITY_NUC

Gapop 10.0 / Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*

2: em_estlm:*

3: em_estln:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hlc:*

9: gb_estl:*

10: gb_est2:*

11: gb_hlc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vit:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	255	13	BJ320065
2	15	100.0	364	10	BE204615
3	15	100.0	370	12	BF518720
4	15	100.0	380	9	AJ503983
5	15	100.0	386	12	BF116561
6	15	100.0	404	10	AW209329

7	15	100.0	409	9	AL373362	AL373362
8	15	100.0	418	12	BF519247	BF519247
9	15	100.0	421	14	BQ140289	BQ140289
10	15	100.0	426	10	AW911108	AW911108
11	15	100.0	429	10	AW207985	AW207985
12	15	100.0	438	10	AM271554	AM271554
13	15	100.0	443	10	AM321427	AM321427
14	15	100.0	451	13	BT72170	BT72170
15	15	100.0	459	13	BB862529	BB862529
16	15	100.0	469	9	AJ503524	AJ503524
17	15	100.0	476	12	BF454382	BF454382
18	15	100.0	477	9	AL381682	AL381682
19	15	100.0	481	12	BG448249	BG448249
20	15	100.0	490	10	BE203104	BE203104
21	15	100.0	498	10	BE203605	BE203605
22	15	100.0	510	12	BF520604	BF520604
23	15	100.0	514	10	AM559351	AM559351
24	15	100.0	520	12	BF634953	BF634953
25	15	100.0	523	12	BF645970	BF645970
26	15	100.0	542	12	BF320644	BF320644
27	15	100.0	583	17	BH084990	BH084990
28	15	100.0	612	12	BG448073	BG448073
29	15	100.0	620	10	BB631108	BB631108
30	15	100.0	623	10	AM775920	AM775920
31	15	100.0	627	12	BF005244	BF005244
32	15	100.0	631	10	BB636948	BB636948
33	15	100.0	632	10	BE317448	BE317448
34	15	100.0	637	10	AM775304	AM775304
35	15	100.0	644	10	AM776844	AM776844
36	15	100.0	651	13	BJ314563	BJ314563
37	15	100.0	651	13	BJ320048	BJ320048
38	15	100.0	653	12	BG451772	BG451772
39	15	100.0	655	12	BF520599	BF520599
40	15	100.0	655	13	BT309270	BT309270
41	15	100.0	658	13	BT264457	BT264457
42	15	100.0	659	14	BQ139038	BQ139038
43	15	100.0	660	12	BG586431	BG586431
44	15	100.0	662	10	AM694259	AM694259
45	15	100.0	662	12	BG452657	BG452657

ALIGNMENTS

RESULT 1
BJ320065/c

LOCUS
DEFINITION
BJ320065 Y. Ogihara unpublished cDNA library, whole Triticum aestivum

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BJ320065.1 GI:20123819
EST.
Bread wheat.
Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 255)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-1
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin1@genes.nig.ac.jp

FEATURES
source
Location/Qualifiers
1..255
/organism="Triticum aestivum"
/cultur="Chinese Spring"
/db_xref="taxon:4565"

PR reducing incidence of restenosis
XX
PS Claim 11; Page 22; 29pp; English.
XX
CC This sequence represents an antisense oligonucleotide directed against
CC rat Egr-1 (an early growth response gene product) that can be used in the
CC method of the invention. The method is for inhibiting the proliferation
CC of cells, and comprises inhibiting induction or decreasing expression of
CC Egr-1, or decreasing the nuclear accumulation or activity of the Egr-1
CC gene product. The method can be used to inhibit proliferation of cells,
CC migration of cells to sites of injury and remodelling of vascular wall
CC associated with atherosclerosis or restenosis and especially to reduce
CC the incidence of restenosis by administration of an agent effective in
CC the method.
XX
SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 other:
Query Match 100.0%; Score 15; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGGCCGCTGCCAT 15
DB 1 CTTGGCCGCTGCCAT 15
RESULT 2
AA74448
ID AAA74448 standard; DNA; 15 BP.
AC AAA74448;
XX
DT 30-NOV-2000 (first entry)
XX
DE Rat AS2 sequence.
XX
KM Rat; Egr-1; NGFI-A; transcription factor; DNazyme;
KM vascular smooth muscle cell; post-angioplasty restenosis;
KM vein graft failure; transplant coronary disease; atherosclerosis;
KM cerebrovascular infarction; stroke; myocardial; heart attack;
KM hypertension; peripheral vascular; gangrene; neoplasia; ss.
XX
OS Rattus sp.
XX
PN WO200042173-A1.
XX
PD 20-JUL-2000.
XX
PF 11-JAN-2000; 2000MO-AU00011.
XX
PR 11-JAN-1999; 99AU-0008103.
XX
PA (UNIX) UNISEARCH LTD.
XX
PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.
XX
PI Atkins DG, Baker AR, Khachigian LM;
XX
DR WPI; 2000-476054/41.
XX
PT DNazyme for treating conditions associated with proliferation or
PT migration of cells e.g. post-angioplasty restenosis, vein graft failure
PT and hypertension cleaves mRNA molecules encoding Egr-1 -
XX
PS Disclosure; Page 5; 62pp; English.
XX
CC Egr-1 (also known as Egr-1 and NGFI-A) is a transcription factor. Egr-1
CC binds to the promoters of genes whose products influence cell movement
CC and replication in the artery wall. DNA-based enzymes (DNazymes), have
CC been developed in the present invention, which can cut Egr-1 mRNA with
CC high efficiency and specificity, resulting in Egr-1 activity inhibition
CC in vascular smooth muscle cells. The DNazymes can be used to inhibit
CC EGR-1 activity in cells, inhibit proliferation or migration of cells and
CC to treat a condition associated with cell proliferation or migration e.g.

CC post-angioplasty restenosis, vein graft failure, transplant coronary
CC disease and complications associated with atherosclerosis e.g.
CC cerebrovascular infarction (stroke), myocardial infarction (heart
CC attack), hypertension or peripheral vascular disease e.g. gangrene of the
CC extremities. The cells which are treated are vascular cells, preferably
CC smooth muscle or endothelial cells or cells involved in neoplasia. The
CC present sequence is rat AS2. This sequence was used to assay the activity
CC of the DNazymes of the present invention.
XX
SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 other:
Query Match 100.0%; Score 15; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGGCCGCTGCCAT 15
DB 1 CTTGGCCGCTGCCAT 15
RESULT 3
AAF85119
ID AAF85119 standard; DNA; 15 BP.
AC AAF85119;
XX
DT 09-JUL-2001 (first entry)
XX
DE Antisense oligonucleotide which targets an EGR gene.
XX
KM Early growth response factor; EGR; tumour cell; tumour; DNazyme;
KM antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
KM skin carcinoma; breast tumour; ss.
XX
OS Synthetic.
XX
PN WO200130394-A1.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000MO-AU01315.
XX
PR 26-OCT-1999; 99AU-0003676.
XX
PA (UNIX) UNISEARCH LTD.
XX
PI Khachigian LM;
XX
DR WPI; 2001-300428/31.
XX
PT Treating tumors including prostate tumour, breast tumour, skin carcinoma,
PT comprises administering agent which inhibits induction or decreases
PT expression of early growth response factor-1 -
XX
PS Claim 8; Page 49; 80pp; English.
XX
CC The present sequence represents an antisense oligonucleotide, which
CC targets an early growth response factor (EGR) gene. The specification
CC describes a method for inhibiting the growth or proliferation of a tumour
CC cell and treating tumours. The method comprises contacting a tumour cell
CC or administering to a subject, an agent which inhibits induction,
CC decreases expression or which decreases the nuclear accumulation or
CC activity of EGR. The agent is a DNazyme or an antisense oligonucleotide.
CC The method is useful for treating solid tumours, including prostate
CC tumours, hepatocellular carcinoma, skin carcinoma or breast tumours.
XX
SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 other:
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGGCCGCTGCCAT 15

ATTORNEY/AGENT INFORMATION:
NAME: Corder, Timothy S.
REGISTRATION NUMBER: 38,414
REFERENCE/DOCKET NUMBER: UROC:007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-626-169-12

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 2; Length 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 15 CTGGCCGCGGCCCAT 1

RESULT 9
US-09-164-907-12/c
Sequence 12, Application US/09164907A
Patent No. 6090559
GENERAL INFORMATION:
APPLICANT: RUSSELL, DAVID W.
APPLICANT: THIGPEN, ANICE E.
TITLE OF INVENTION: BIOMARKERS FOR DETECTION, DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER
FILE REFERENCE: UROC:021
CURRENT APPLICATION NUMBER: US/09/164,907A
CURRENT FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 08/626,169
EARLIER FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-164-907-12

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 3; Length 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 15 CTGGCCGCGGCCCAT 15

RESULT 10
US-08-760-075A-15/c
Sequence 15, Application US/08760075A
Patent No. 5942429
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
APPLICANT: MUELLNER, Stefan
APPLICANT: BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..612
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..612
US-08-760-075A-15

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 2; Length 612;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 339 CTGGCCGCGGCCCAT 325

RESULT 11
US-09-338-546-15/c
Sequence 15, Application US/09338546
Patent No. 6251645
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
APPLICANT: MUELLNER, Stefan
APPLICANT: BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995

RESULT 14
US-08-855-714-1
Sequence 1, Application US/08855714
Patent No. 5939075
GENERAL INFORMATION:
APPLICANT: Houns, Huo-Shu H.
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: MUTANTS OF BRUCELLA MELITENSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran, Esq.
STREET: HQ USAMRDC, Dept. of Army, Fort Detrick
CITY: Frederick
STATE: MD
COUNTRY: US
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,714
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/334,129
FILING DATE: 04-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: 08/143,692
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BRUCELLA MELITENSIS
US-08-855-714-1
Query Match 89.3%; Score 13.4; DB 2; Length 1920;
Best Local Similarity 93.3%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTGGCCGCTGCCAT 15
DB 409 CATGGCCGCTGCCAT 423

RESULT 15
US-07-872-644-5
Sequence 5, Application US/07872644
Patent No. 5389527
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,644
FILING DATE: 19920420
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5389527and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2291 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 100..1689
US-07-872-644-5
Query Match 89.3%; Score 13.4; DB 1; Length 2291;
Best Local Similarity 93.3%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTGGCCGCTGCCAT 15
DB 858 CTTGGCCGCTGCCAT 872

Search completed: December 16, 2002, 14:16:48
Job time : 69 secs

directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XL10R cells. Note: EST may be of fungal origin."

BASE COUNT 120 a 74 c 112 g 112 t

Query Match 100.0%; Score 15; DB 12; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCCCGCTGCCAT 15
|||||
DB 275 CTTGCCCGCTGCCAT 261

RESULT 9

BOI40289/c

LOCUS BOI40289 421 bp mRNA linear EST 26-APR-2002
DEFINITION NF034A02PH1017 Phoma-infected Medicago truncatula cDNA clone
NF034A02PH 5', mRNA sequence.

ACCESSION BOI40289

VERSION BOI40289.1 GI:20276415

KEYWORDS EST.

SOURCE barrel medic.
ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 421)

WATSON,B.S., SHIH,H.-S., LOPEZ-MEYER,M., SCOTT,A.D., HARRIS,A.R., GONZALES,R.A., BELL,C.J., IMMAN,J.T., MAUGH,M.E., SULLIVAN,J.P., MAY,G.D. and PALVA,N.L.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula Phoma-infected library
Unpublished (2002)

JOURNAL COMMENT

Contact: Palva NL
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nlpalva@noble.org

Insert Length: 421
Plate: 034 row: A column: 02
Seq primer: TCACACAGGAACACCTATGAC.

FEATURES

source

1..421
/organism="Medicago truncatula"
/db_xref="taxon:3880"

/clone_1lb="Phoma-infected"

/tissue_type="leaf"

/dev_stage="Pathogen-induced, Young trifoliolate"

/note="Vector: pBluescript SK(-); Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-ZAP XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using Ex-Assist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOIR cells."

BASE COUNT

121 a 84 c 98 g 116 t 2 others

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCCCGCTGCCAT 15
|||||
DB 360 CTTGCCCGCTGCCAT 346

RESULT 10

AW911108/c

LOCUS AW911108 426 bp mRNA linear EST 25-MAY-2000
DEFINITION ur82g09.y1 NCI-CGAP Mam6 Mus musculus cDNA clone IMAGE:3156832 5' similar to gb:M20157 Mouse Egr-1 mRNA, complete cds (MOUSE);, mRNA sequence.

ACCESSION AW911108
VERSION AW911108.1 GI:8076354

KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 426)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/lresources.shtml

MGI:1059588
Seq primer: -40RP from Gibco

High quality sequence stop: 400.
Location/Qualifiers

FEATURES

source

1..426

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone_1lb="IMAGE:3156832"

/clone_1lb="NCI-CGAP Mam6"

/sex="female, virgin"

/tissue_type="infiltrating ductal carcinoma"

/dev_stage="5 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: PCMV-SpOrf6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 86 a 150 c 127 g 63 t

Query Match 100.0%; Score 15; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCCCGCTGCCAT 15
|||||
DB 136 CTTGCCCGCTGCCAT 122

RESULT 11

AW207985/c

LOCUS AW207985 429 bp mRNA linear EST 07-SEP-2000
DEFINITION M11006e DSIR Medicago truncatula cDNA clone IR58, mRNA sequence.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/HLN at:
www.bio.lnlnl.gov/db/rrp/image/image.html

MGI:1024625
 Seq primer: -40RP from 61bco
 High quality sequence stop: 413.
 Location/Qualifiers

FEATURES

source

1.443
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_image="263117"
 /clone_11b="NCI-CGAP_Mam6"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT

75 a 182 c 122 g 64 t

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 443;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15

Db 253 CTTGGCCGCTGCCAT 239

RESULT 14

BI272170 451 bp mRNA linear EST 18-JUL-2001
 LOCUS NF021E02FL1018 Developing flower Medicago truncatula cDNA clone

DEFINITION

NF021E02FL 5', mRNA sequence.

ACCESSION

BI272170

VERSION

BI272170

KEYWORDS

EST.

SOURCE

barrel medic.

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE

1 (bases 1 to 451)

AUTHORS

Torres-Jerez,T., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
 Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

JOURNAL

Medicago truncatula flower library

COMMENT

Unpublished (2001)

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7391

Fax: 580 221 7380

Email: gdmay@noble.org

Insert Length: 451 Std Error: 0.00

Plate: 021 row: E column: 02

Seq primer: TCACACAGGAAACAGCTATGAC.

Location/Qualifiers

1.451

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone_image="NF021E02FL"

/clone_11b="Developing flower"

/tissue_type="Developing flowers"

/dev_stage="Developmentally pooled. Contains a mixture of

BASE COUNT

133 a 83 c 112 g 122 t 1 others

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15

Db 335 CTTGGCCGCTGCCAT 321

RESULT 15

BB862529 459 bp mRNA linear EST 26-NOV-2001
 LOCUS BB862529 RIKEN full-length enriched, pooled cell lines Mus musculus

DEFINITION

CDNA clone G430028C23 5', mRNA sequence.

ACCESSION

BB862529

VERSION

BB862529

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE

1 (bases 1 to 459)

AUTHORS

Akimura,T., Arakawa,T., Carinici,P., Furuno,M., Hanagaki,T., Ishii
 Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
 Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
 Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
 Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
 Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suuki,H., Tagawa
 A., Takahashi,F., Takaku-Akashita,S., Tanaka,T., Tomaru,A., Toyu,T.,
 Watabiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
 2001)

JOURNAL

Unpublished (2001)

COMMENT

Contact: Yoshinori Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suenho-cho, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9226

Email: genome-res@sc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carinici,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

Wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura

S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

very young, developing, fully-opened flowers and flowers
 in early transition into pods."
 /note="Vector: Lambda Zap; cDNA was prepared from polyA+
 enriched, pooled samples of equivalent amounts of total
 RNA from very young, developing, fully-opened flowers and
 flowers transitioning into pods. The cDNA was
 directionally ligated into the Uni-Zap XR vector
 (Stratagene) and packaged using the GigaPack III Gold
 packaging extracts. Phagemids containing cDNA inserts were
 in vivo excised from the recombinant Uni-Zap XR vector
 using Exassist helper phage and the E. coli strain
 XL1-Blue MRF' (Stratagene). Excised plasmids were plated
 using SOLR cells."

Computer-based methods for the mouse full-length cDNA

KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis; gene; ss.
 OS Homo sapiens.
 XX W0200192523-A2.
 PN 06-DEC-2001.
 PD 29-MAY-2001; 2001WO-US10836.
 PF 30-MAY-2000; 2000US-206132P.
 PR 29-AUG-2000; 2000US-228716P.
 XX (CURA-) CURAGEN CORP.
 PA Shinkets RA, Leach MD;
 PI WPI; 2002-106308/14.
 DR P-PSDB; ABP01278.
 DR
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders
 PS Disclosure; SEQ ID 2537; 1037bp; English.
 XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 501 BP; 81 A; 139 C; 177 G; 104 T; 0 other;
 Query Match 93.3%; Score 14; DB 24; Length 501;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 0Y 1 CTTGGCCGCTGCCA 14
 |||||
 Db 310 CTTGGCCGCTGCCA 297

Search completed: December 16, 2002, 12:41:33
 Job time : 304 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 12:41:44 ; Search time 89 Seconds

(without alignments)
66,651 Million cell updates/sec

Title: US-09-648-389A-1

Sequence: 1 cttggccgcgtccat 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCRTS_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	433	US-09-960-352-1555	Sequence 1555, Ap
2	15	100.0	3112	US-09-917-800A-1543	Sequence 1543, Ap
3	13.4	89.3	152	US-09-974-300-5464	Sequence 5464, Ap
4	13.4	89.3	157	US-09-864-761-27552	Sequence 27552, A
5	13.4	89.3	255	US-09-864-761-20348	Sequence 20348, A
6	13.4	89.3	255	US-09-864-761-21839	Sequence 21839, A
7	13.4	89.3	265	US-09-923-876-2313	Sequence 2313, Ap
8	13.4	89.3	273	US-09-923-876-4805	Sequence 4805, Ap
9	13.4	89.3	349	US-09-960-352-1856	Sequence 1856, A
10	13.4	89.3	414	US-09-960-352-11961	Sequence 11961, A
11	13.4	89.3	425	US-09-960-352-10722	Sequence 10722, A
12	13.4	89.3	454	US-09-864-761-1580	Sequence 1580, Ap
13	13.4	89.3	454	US-09-864-761-16568	Sequence 16568, A
14	13.4	89.3	480	US-09-864-761-10916	Sequence 10916, A
15	13.4	89.3	480	US-09-974-300-5449	Sequence 5449, Ap
16	13.4	89.3	579	US-09-864-761-15317	Sequence 15317, A
17	13.4	89.3	681	US-09-815-242-6787	Sequence 6787, Ap
18	13.4	89.3	775	US-09-910-943-62	Sequence 62, Appl
19	13.4	89.3	1026	US-09-974-300-6635	Sequence 6635, Ap

20	13.4	89.3	1593	US-09-814-777A-31	Sequence 31, Appl
21	13.4	89.3	1926	US-10-024-632-5	Sequence 5, Appl1
22	13.4	89.3	2291	US-09-883-825-5	Sequence 16, Appl1
23	13.4	89.3	2656	US-09-883-825-16	Sequence 320, Appl
24	13.4	89.3	3132	US-09-736-457-320	Sequence 320, Appl
25	13.4	89.3	3132	US-09-802-941-320	Sequence 3721, Ap
26	13.4	89.3	3132	US-09-880-107-3721	Sequence 151, Appl
27	13.4	89.3	3984	US-09-954-531-151	Sequence 61, Appl
28	13.4	89.3	4021	US-10-002-600-40	Sequence 555, App
29	13.4	89.3	4559	US-09-919-172-61	Sequence 128, App
30	13.4	89.3	4559	US-10-044-090-555	Sequence 81, Appl
31	13.4	89.3	12421	US-09-989-920-128	Sequence 229, Appl
32	13.4	89.3	15747	US-09-070-927A-81	Sequence 30, Appl
33	13.4	89.3	17082	US-09-070-927A-81	Sequence 580, Appl
34	13.4	89.3	25	US-09-840-479-30	Sequence 11819, A
35	13.4	89.3	31	US-09-801-274-580	Sequence 632, App
36	13.4	86.7	271	US-09-878-574-11159	Sequence 961, App
37	13.4	86.7	272	US-09-923-876-1383	Sequence 961, App
38	13.4	86.7	324	US-09-920-300A-632	Sequence 10566, A
39	13.4	86.7	324	US-10-033-528-632	Sequence 8849, Ap
40	13.4	86.7	324	US-10-033-528-632	Sequence 598, App
41	13.4	86.7	324	US-10-033-528-632	Sequence 606, App
42	13.4	86.7	393	US-09-960-352-10566	
43	13.4	86.7	408	US-09-960-352-10566	
44	13.4	86.7	445	US-09-764-864-598	
45	13.4	86.7	468	US-10-046-935-606	

ALIGNMENTS

RESULT 1
US-09-960-352-1555/c
Sequence 1555 Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathaiagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION A
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1555
LENGTH: 433
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 07-LIB34-039-Q1-EL-B3
US-09-960-352-1555

Query Match 100.0%; Score 15; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCGTCCAT 15
DB 24 CTTGGCCGCGTCCAT 10

RESULT 2
US-09-917-800A-1543/c
Sequence 1543 Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castile, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arc0067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 843 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-040-548-9

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 843;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCGCTGCCAT 15
DB 15 CTGGCCGCTGCCAT 1

RESULT 3
US-08-466-344-9/c
Sequence 9, Application US/08466344
Patent No. 5773583
GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
NUMBER OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,548
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arc0067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 843 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-466-344-9

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 843;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCGCTGCCAT 15
DB 15 CTGGCCGCTGCCAT 1

RESULT 4
US-08-224-482-1/c
Sequence 1, Application US/08224482
Patent No. 5837692
GENERAL INFORMATION:
APPLICANT: Mercola, Dan
ATTORNEY/AGENT INFORMATION:
NAME: Adamson, Eileen D.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: PDGF by Mammalian EGR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,482
FILING DATE: 07-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ME 9913
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 370..1858
US-08-224-482-1

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 3068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCGCTGCCAT 15
DB 273 CTGGCCGCTGCCAT 259

RESULT 5
US-08-040-548-15/c
Sequence 15, Application US/08040548
Patent No. 5763209
GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
NUMBER OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67

OY 1 CTGGCGCGTGCAT 15
||||| |||||||
DB 142 CTGGCGCGTGCAT 156

RESULT 5
US-09-864-761-20348/c
Sequence 20348, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aesomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20348
LENGTH: 255
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007263.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.88
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.92

OTHER INFORMATION: NT HIT: X74507.1, EVALU 6.10e-01
OTHER INFORMATION: SWISSPROT HIT: P56558, EVALU 8.70e+00
US-09-864-761-20348
Query Match 89.3%; Score 13.4; DB 10; Length 255;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CTGGCGCGTGCAT 15
||||| |||||||
DB 104 CTGGCGCGTGCAT 90

RESULT 6
US-09-864-761-31839/c
Sequence 31839, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aesomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31839
LENGTH: 255
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007263.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.5

Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCGCTGCCAT 15
|||||||
Db 49 CTTGGCGATGCCAT 35

Search completed: December 16, 2002, 14:18:28
Job time : 89 secs



Creation date: 12-02-2003

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Team: OIPEBackFileIndexing

Dossier: 09648389

Legal Date: 03-12-2003

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Total number of pages: 3

Remarks:

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